

What is claimed is:

1. Isolated polynucleotide containing a polynucleotide sequence coding for the sucC- and/or sucD-gene, selected from the group comprising
  - 5 a) Polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,
  - b) Polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that  
10 contains the amino acid sequence of SEQ ID No. 3,
  - c) Polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to that of the amino acid sequence of SEQ ID No. 2,
  - 15 d) Polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to that of the amino acid sequence of SEQ ID No. 3,
  - e) Polynucleotide that is complementary to the  
20 polynucleotides of a), b), c) or d), and
  - f) Polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequences of a), b), c), d) or e),the polypeptide preferably having the activity of  
25 succinyl-CoA synthetase.
2. Polynucleotides according to claim 1, wherein the polynucleotide is a preferably recombinant DNA that is replicable in coryneform bacteria.
3. Polynucleotides according to claim 1, wherein the  
30 polynucleotide is a RNA.

4. Polynucleotides according to claim 2, containing the nucleic acid sequence as shown in SEQ ID NO 1.
5. Replicable DNA according to claim 2, containing
  - (i) the nucleotide sequence shown in SEQ ID NO 1, or
  - 5 (ii) at least one sequence that corresponds to the sequences (i) within the region of degeneration of the genetic code, or
  - (iii) at least one sequence that hybridizes with the sequences that are complementary to the
  - 10 sequences (i) or (ii) , and optionally
  - (iv) functionally neutral sense mutations in (i).
6. Replicable DNA according to claim 5, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.
- 15 7. Polynucleotide sequence according to claim 1 that codes for a polypeptide that contains the amino acid sequence shown in SEQ ID No. 2.
8. Coryneform bacteria in which the sucC- and/or sucD-gene is/are attenuated.
- 20 9. Process for producing L-amino acids, in particular L-lysine and/or L-glutamate, wherein the following steps are carried out:
  - a) fermentation of the bacteria producing the
  - 25 desired L-amino acid, in which first of all the sucC- and/or sucD-gene or nucleotide sequences coding therefor are attenuated, in particular switched off;
  - b) enrichment of the L-amino acid in the medium or in the bacterial cells, and
  - 30 c) isolation of the L-amino acid.

10. Process according to claim 9, wherein bacteria are used in which in addition further genes of the biosynthesis pathway of the desired L-amino acid are enhanced.
- 5 11. Process according to claim 9, wherein bacteria are used in which the metabolic pathways that reduce the formation of the desired L-amino acid are at least partially switched off.
- 10 12. Process according to claim 9, wherein the expression of the polynucleotide(s) that codes for the sucC- and/or sucD-genes is attenuated, in particular is switched off.
- 15 13. Process according to claim 9, wherein the catalytic properties of the polypeptide (enzyme protein) for which the polynucleotides sucC and sucD code are reduced.
- 20 14. Process according to claim 9, wherein for the production of L-amino acids microorganisms are fermented in which at the same time one or more of the genes selected from the following group is/are enhanced and/or overexpressed:
  - 14.1 the dapA-gene coding for dihydrodipicolinate synthase,
  - 14.2 the pyc-gene coding for pyruvate carboxylase,
  - 25 14.3 the gap-gene coding for glyceraldehyde-3-phosphate dehydrogenase,
  - 14.4 the gene tpi coding for triose phosphate isomerase,
  - 30 14.5 the gene pgk coding for 3-phosphoglycerate kinase,

- 14.6 the mqo-gene coding for malate:quinone  
oxidoreductase,
- 14.7 the lysE-gene coding for L-lysine export,
- 5 14.8 the gene lysC coding for a feedback resistant  
aspartate kinase,
- 14.9 the gene zwal coding for the Zwal-protein.
15. Process according to claim 9, wherein for the  
production of L-amino acids coryneform microorganisms  
are fermented, in which at the same time one or more  
10 of the genes selected from the following group is/are  
attenuated:
- 15.1 the gene pck coding for phosphoenol pyruvate  
carboxykinase,
- 15.2 the gene pgi coding for glucose-6-phosphate  
15 isomerase,
- 15.3 the gene poxB coding for pyruvate-oxidase,
- 15.4 the gene zwa2 coding for the Zwa2-Protein.
16. Coryneform bacteria containing a vector that carries  
parts of the polynucleotide according to claim 1, but  
20 at least 15 successive nucleotides of the claimed  
sequence.
17. DNA derived from coryneform bacteria that code for  
SucC proteins, whose amino acid sequence (SEQ ID No.  
2) contains one or more replacements selected from the  
25 group: replacement at position 22 by any other  
proteinogenic amino acid except L-proline, replacement  
at position 44 by any other proteinogenic amino acid  
except glycine, and replacement at position 170 by any  
other proteinogenic amino acid except L-alanine.

18. DNA according to claim 17, wherein this codes for SucC proteins whose amino acid sequences contain one or more replacements selected from the group: L-proline at position 22 by L-serine, glycine at position 44 by L-glutamic acid, and L-alanine at position 170 by L-threonine.  
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19. DNA according to claim 18, wherein this codes for a SucC protein whose amino acid sequence contains L-serine at position 22, L-glutamic acid at position 44, and L-threonine at position 170, as illustrated in SEQ ID No.5.  
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20. DNA according to claim 17, wherein this contains the nucleobase thymine at position 64, the nucleobase adenine at position 131, and the nucleobase adenine at position 508, as illustrated in SEQ ID No 4.  
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21. Coryneforme bacteria that contain a DNA according to claim 17, 18, 19 or 20.
22. Integration vector pCRBluntsucCint, that
  - 22.1 carries a 0.55 kb long internal fragment of the sucC-gene,  
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  - 22.2 whose restriction map is reproduced in Fig. 1, and
  - 22.3 that in the E. coli strain TOP10/pCRBluntsucCint has been filed under No. DSM 13750 at the German  
25 Collection for Microorganisms and Cell Cultures.
23. Plasmid vector pK18mobsacBsucDdel that
  - 23.1 carries a sucD-gene containing a deletion,
  - 23.2 whose restriction map is reproduced in Fig. 2, and

23.3 that in the E. coli strain DH5 $\alpha$ mcr/  
pK18mobsacBsucDdel has been filed under No. DSM  
13749 at the German Collection for Microorganisms  
and Cell Cultures.

- 5 24. Process according to one or more of the preceding  
claims, wherein microorganisms of the type  
Corynebacterium glutamicum are used.
- 10 25. Process for detecting RNA, cDNA and DNA in order to  
isolate nucleic acids and/or polynucleotides or genes  
that code for succinyl-CoA synthase or that have a  
high degree of similarity to the sequence of the sucC-  
and/or sucD-gene, wherein the polynucleotide  
containing the polynucleotide sequences according to  
claims 1, 2, 3 or 4, is used as hybridization probe.